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**P27449**

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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

### General information about the entry

Entry name	<b>VATL_HUMAN</b>
Primary accession number	<b>P27449</b>
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 23, August 1992
Sequence was last modified in	Release 23, August 1992
Annotations were last modified in	Release 41, June 2002

### Name and origin of the protein

Protein name	<b>Vacuolar ATP synthase 16 kDa proteolipid subunit</b>
Synonym	<b>EC <u>3.6.3.14</u></b>
Gene name	<b>ATP6V0C or ATP6L or ATP6C or ATP1L</b>
From	<b>Homo sapiens (Human) [TaxID: 9606]</b>
Taxonomy	<b>[Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eularchia; Primates; Catarrhini; Hominidae; Homo]</b>

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
MEDLINE#91239553; PubMed #1709739; [NCBI, EMBL, EBI, Israel, Japan]  
Gillespie G.A.J., Somlo S., Germano G.G., Weinstein D., Reekers S.T.;  
"CpG island in the region of an autosomal dominant polycystic kidney disease locus defines the 5' end of a gene encoding  
a putative proton channel";  
Proc. Natl. Acad. Sci. U.S.A. 88:4289-4293(1991).
- [2] SEQUENCE FROM NUCLEIC ACID.  
TISSUE Brain, Muscle, and Skin;  
Strausberg R.;  
Submitted (JUN-2001) to the EMBL, GenBank DDBJ databases.

## Comments

- **FUNCTION:** PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL V<sub>0</sub> COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
- **CATALYTIC ACTIVITY:**  $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) \rightarrow \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$ .
- **SUBUNIT:** V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC V<sub>1</sub> COMPLEX (MAIN COMPONENTS: SUBUNITS A, B, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V<sub>0</sub> PROTON PORE COMPLEX (MAIN COMPONENT, THE PROTEOLIPID PROTEIN WHICH IS PRESENT AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).
- **SUBCELLULAR LOCATION:** Integral membrane protein. Vacuolar
- **MISCELLANEOUS:** THIS SUBUNIT BINDS DICYCLOHEXYL CARBODIIMIDE (DCDD) WHICH INHIBITS THE ATPASE.
- **SIMILARITY:** BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.

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**Cross-references**

	M62762: AAA60039.1. - [ <a href="#">EMBL</a> ] [ <a href="#">GenBank</a> ] [ <a href="#">DDBJ</a> ] [ <a href="#">CodingSequence</a> ]
	BC004537: AAH04537.1. - [ <a href="#">EMBL</a> ] [ <a href="#">GenBank</a> ] [ <a href="#">DDBJ</a> ] [ <a href="#">CodingSequence</a> ]
EMBL	BC007389: AAH07389.1. - [ <a href="#">EMBL</a> ] [ <a href="#">GenBank</a> ] [ <a href="#">DDBJ</a> ] [ <a href="#">CodingSequence</a> ]
	BC007759: AAH07759.1. - [ <a href="#">EMBL</a> ] [ <a href="#">GenBank</a> ] [ <a href="#">DDBJ</a> ] [ <a href="#">CodingSequence</a> ]
	BC009290: AAH09290.1. - [ <a href="#">EMBL</a> ] [ <a href="#">GenBank</a> ] [ <a href="#">DDBJ</a> ] [ <a href="#">CodingSequence</a> ]
PIR	A39367: A39367.
Genew	<a href="#">HGNC:355</a> : ATP6V0C.
CleanEx	<a href="#">HGNC:355</a> : ATP6V0C.
MIM	108745 [ <a href="#">NCBI</a> ] [ <a href="#">E3L</a> ].
GeneCards	<a href="#">ATP6V0C</a> .
GeneLynx	<a href="#">ATP6V0C</a> : Homo sapiens.
SOURCE	<a href="#">ATP6V0C</a> : Homo sapiens.
Ensembl	P27449, Homo sapiens. [ <a href="#">Entry</a> ] [ <a href="#">ConfigView</a> ]
	<a href="#">IPF00179</a> : ATPase_Csub.
InterPro	<a href="#">IPF00145</a> : Vac_ATPsynth_Csub. <a href="#">Graphical view of domain structure</a> .
Pfam	<a href="#">P10013</a> : ATP-synth_C:2.
PRINTS	<a href="#">P10013</a> : VACATPASE
TIGRFAMs	<a href="#">TIGR0100</a> : V_ATP_synth_C:1.
ProDom	<a href="#">[Domain structure - List of seq. sharing at least 1 domain]</a> .
BLOCKS	<a href="#">P27449</a> .
ProtoNet	<a href="#">P27449</a> .
ProtoMap	<a href="#">P27449</a> .
PRESAGE	<a href="#">P27449</a> .
DIP	<a href="#">P27449</a> .
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**Keywords**

Hydrolase; Hydrogen ion transport; ATP synthesis; Transmembrane.

**Features**

Key	From	To	Length	Description
DOMAIN	1	10	10	LUMENAL ( <i>POTENTIAL</i> ) .
TRANSMEM	11	12	23	<i>POTENTIAL</i> .
DOMAIN	34	55	22	CYTOPLASMIC ( <i>POTENTIAL</i> ) .
TRANSMEM	56	56	21	<i>POTENTIAL</i> .
DOMAIN	77	92	16	LUMENAL ( <i>POTENTIAL</i> ) .
TRANSMEM	93	114	22	<i>POTENTIAL</i> .
DOMAIN	115	126	12	CYTOPLASMIC ( <i>POTENTIAL</i> ) .
TRANSMEM	127	152	26	<i>POTENTIAL</i> .
DOMAIN	153	155	3	LUMENAL ( <i>POTENTIAL</i> ) .
BINDING	130	139		DICYCLOHEXYLCARBODIIMIDE ( <i>POTENTIAL</i> ) .



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**Sequence information**

Length: 155 AA Molecular weight: 15736 Da CRC64: 91141854A0492A5B [This is a checksum on the sequence]

```
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MSESKSGPEY ASFFAVMGAS AAMVFSALGA AYGTAKSGTG IAAMSVMRPE QIMKSIIPVV
      70      80      90     100     110     120
MAGITATYGL VVAVLIANSI NDDISLYKSF LQLGAILSVG LSGLAAGFAI GTVGDAGVKG
     130     140     150
TAQQPRLEVG MILILTFAEV LGLYGLIVAL ILSTK
```

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Direct BLAST submission at [NCBI \(Bethesda, USA\)](#)



[ScanProsite](#), [MotifScan](#)



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## P23956

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### General information about the entry

Entry name: **VATL\_BOVIN**  
 Primary accession number: **P23956**  
 Secondary accession numbers: None  
 Entered in Swiss-Prot in: Release 21, March 1992  
 Sequence was last modified in: Release 21, March 1992  
 Annotations were last modified in: Release 41, June 2002

### Name and origin of the protein

Protein name: **Vacuolar ATP synthase 16 kDa proteolipid subunit**  
 Synonym: **EC 3.6.3.14**  
 Gene name: **ATP6V0C or ATP6L or ATP6C**  
 From: **Bos taurus (Bovine) [TaxID: 9913]**  
 Taxonomy: **Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.**

### References

- [1] SEQUENCE FROM NUCLEIC ACID.  
 MEDLINE: 88289753; PubMed: 2456571; [NCBI, Expasy, EBI, Israel, Japan]  
 Mandel M., Moriyama Y., Holmes J.D., Pan Y.-C.T., Nelson H., Nelson N.;  
 "cDNA sequence encoding the 16-kDa proteolipid of chromaffin granules implies gene duplication in the evolution of H<sup>+</sup>-ATPases";  
 Proc. Natl. Acad. Sci. U.S.A. 85:5521-5524(1988).
- [2] REVISIONS.  
 Nelson N.;  
 Submitted (JUN-1988) to the EMBL, GenBank, DDBJ databases.
- [3] SEQUENCE OF 7-26.  
**TISSUE**-Brain;  
 MEDLINE: 89338721; PubMed: 2527163; [NCBI, Expasy, EBI, Israel, Japan]  
 Dermietzel R., Voelker M., Hwang L.K., Benborn R.F., Meyer H.H.;  
 "A 16 kDa protein co-isolating with gap junctions from brain tissue belonging to the class of proteolipids of the vacuolar H<sup>+</sup>-ATPases";  
 FEBS Lett. 253:1-5(1989).

### Comments

- **FUNCTION:** PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL V0 COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
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- **SUBCELLULAR LOCATION:** Integral membrane protein. Vacuolar.
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### Cross-references

EMBL J03835; AAA30397.1; -[EMBL][GenBank][DDBJ][CoDingSequence]  
 PIR A31320; PNBOV6.  
 S05209; S05209.  
 IPR002379; ATPase\_Csub.  
 InterPro IPR000247; Vac\_ATPsynth\_Csub.  
 Graphical view of domain structure.  
 Pfam PF00137; ATP-synth\_C; 2.  
 PRINTS PR00122; VACATPASE.  
 TIGRFAMs TIGR01109; V\_ATP\_synth\_C; 1.  
 ProDom [Domain structure - List of seq. sharing at least 1 domain].  
 BLOCKS P23956.  
 ProtoNet P23956.  
 ProtoMap P23956.  
 PRESAGE P23956.  
 DIP P23956.  
 ModBase P23956.  
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### Keywords

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### Features

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DOMAIN	1	10	10	LUMENAL (POTENTIAL).
TRANSMEM	11	31	21	POTENTIAL.
DOMAIN	34	55	22	CYTOPLASMIC (POTENTIAL).
TRANSMEM	56	76	21	POTENTIAL.
DOMAIN	77	92	16	LUMENAL (POTENTIAL).
TRANSMEM	93	114	22	POTENTIAL.
DOMAIN	115	126	12	CYTOPLASMIC (POTENTIAL).
TRANSMEM	127	147	20	POTENTIAL.
DOMAIN	148	150	3	LUMENAL (POTENTIAL).
BINDING	148	150	3	DICYCLOHEXYLCARBODIIMIDE (POTENTIAL).



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### Sequence information

Length: 155 AA Molecular weight: 15720 Da CRC64: 326B20B5F7D7D607 [This is a checksum on the sequence]

```

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      :      :      :      :      :      :
MSEAKNGPEY ASFFAVMQAS AAMVFSALGA A/GTAKSGTG IAAMSVMRPE MIMKSIIPVV
      70      80      90     100     110     120
      :      :      :      :      :      :
MA3IIAIYGL VVAVLIANSI NKGISLYRSF LQLGAGLSVG LSGLAAGFAI GIVGDAGVRG
     130     140     150
      :      :      :
TAQPPPLPVG MILILIFAEV LGLYGLIVAL ILSTK
  
```

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Direct BLAST submission at NCBI (Bethesda, USA)



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Feature table viewer (Java)



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1	14	vacuolar adj atp adj synthase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:42
2	524	proteolipid	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:42
3	0	(vacuolar adj atp adj synthase) near5 proteolipid	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:42
4	0	(vacuolar adj atp adj synthase) with proteolipid	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:42
5	8	(vacuolar adj atp adj synthase) and proteolipid	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:43
6	0	atp6v0c	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:43
7	0	atp6l	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:43
8	8	atp6c	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:45
9	14	vacuolar near3 atp\$ near3 synthase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:45
10	4	vacuolar near3 atp\$ near3 proteolipid	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003 02 07 10:46